

Jennifer: An Expert System for the Epidemiological Analysis of the Information Generated from a Microbiological Surveillance Network (RVM) in Spain

Isabel C. Munoz, MD PhD¹, Rafael Borrás, MD PhD², Miguel Gobernado, MD PhD³, Francisco Pardo, MD PhD⁴, Joaquin Plazas, MD PhD⁵, Alberto Yaque, MD PhD⁶, Francisco Gonzalez, MD¹, Herme Vanaclocha, MD¹.

¹Area de Epidemiologia, Direccion General de Salud Publica Conselleria de Sanidad, Valencia, Spain, ²Microbiologia, Hosp Clin, Valencia, Spain, ³Microbiologia, HospLaFe, Valencia, Spain, ⁴Microbiologia, Hosp General, Castellon, Spain, ⁵Microbiologia, Hosp General, Alicante, Spain, ⁶Microbiologia, Hosp Vega Baja, Orihuela, Spain

Background

The development of a network connecting five microbiological laboratories from 5 hospitals in La Comunidad Valenciana gives real-time data from microbiological analyses. This data is extensive and it is very difficult to interpret each result independently due to the number of results received each day and because it has to be compared to data stored previously from the same patient.

Methods

After initialization of the system, the process begins by closing all expired cases. It then scans for existing condition records and identifies new test results queued for processing, as shown in the diagram below.

In addition to the tables created for the Microbiological Surveillance Network, several new tables were designed to aid in data analysis:

- **Disease Map:** List of diseases associated with a given test result, microorganism and type of specimen
- **Infection Type:** List of potential infection types, includes columns for infection type, and whether the test is final (does not require further tests to definitively assign case type), the case type associated to each infection type, and the priority assigned to each case type if different types are associated with the same record
- **Infection Map:** List of infection types associated with a given test result, microorganism, and type of specimen. Includes columns indicating whether infection type depends on the test result, whether the infection type is observed in a single test or on an observed increase in a single test result, and in the latter case – the fold-change that is required.
- **Dependencies Map:** List of infection types dependent on an association between a test result and a microorganism. Includes columns indicating the types of tests and specific results required.



Process

- Initialize test result data**

Once the process is initiated, the following data is obtained for each test result:

 - Patient
 - Specimen
 - Test
 - Microorganism
- Obtain the disease**

The disease is identified based on the type of specimen, type of test, and microorganism for which the test was performed using the Disease Map table. If the disease is not found, the result is marked as processed.
- Check for pre-existing condition record**

Each time a disease is associated with a test result, the system checks for a pre-existing record of the disease condition that is associated with the result (condition record). Pre-existing condition records must meet the following criteria:

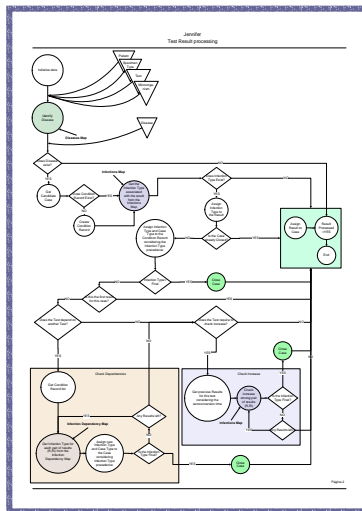
 - Same patient
 - Same disease
 - The time between the condition record and the test result date is not longer than the time of immunity of the disease in days

If a condition record meeting these criteria doesn't exist, a new record is created. If the condition record exists and is closed, the result is added to the record and
- Create a new condition record, patient, disease and test result data are needed. The new condition record will consist of:**

 - Date
 - Patient Identification
 - Disease identification
 - Microorganism identification associated with test result
 - Infection Type
 - Case Type
 - Case confirmation. If the disease needs confirmation, this value will be N. If it does not, the value will be S.
 - Case closure. S indicates the case is closed. By default, this value is N.
- Obtain the infection type**

The infection type is determined using the values for test_id, mic_id, spec_id, res_id (test, microorganism, specimen and result) listed in the Infection Map table.



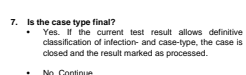
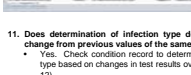
If an infection type cannot be determined from these data, the result is associated with the condition record and marked as processed.



Results

An example of a condition record (infectious mononucleosis) is showed below



- ### Obtain the case type
- Case types are determined that correspond to the infection types associated with each of the test results in the condition record. The case type with the highest priority as listed in the Infection Type table is used to define the case type.
- 
- 
- 
- 
- Is the case type final?
 - Yes. If the current test result allows definitive classification of infection- and case-type, the case is closed and the result marked as processed.
 - No. Continue.
 - Is this the first test result in this condition record?
 - Yes. Mark test result as processed.
 - No. Continue.
 - Does determination of infection type based on a relationship to the result from a different test?
 - Yes. Check Dependences Map table to determine the infection type based on results from different types of tests (step 10).
 - No. Continue to step 11.
 - Determination of infection type based on results from different types of tests.

For each new result R_i scan the condition record for associated test results R_j based on criteria from the Dependences Map table.

 - The R_j test is the same as test_id_first
 - The R_j test is the same as test_id_second
 - The R_j value type is the same as val_id_first
 - The R_j value type is the same as val_id_second

If a valid infection type is assigned, and corresponds to a case type that is final, close the case and mark the result as processed. If the assigned infection type is not final, continue to step 11.
 - Does determination of infection type depend on a change from previous values of the same test?
 - Yes. Check condition record to determine infection type based on changes in test results over time (step 12).
 - No. Mark the result as processed.
 - Determination of infection type based on changes in test results over time.

Obtain previous results R_i in the condition record that meet the following parameters with respect to the current value R₀.

 - Same patient
 - Same microorganism
 - Same test
 - Same specimen
 - Same laboratory
 - The time elapsed from R_i to R₀ is not longer than the seroconversion time (5 (weeks for default))

For each previous result R_i that meets these criteria, calculate the fold-change between the previous result and the current result (R₀/R_i). Assign infection type from the Infection Map table based on the calculated fold-change. If infection type corresponds to a case type that is final, close the case and mark the result as processed.
 - Final result

If at the end of this process, a final infection type cannot be assigned to the result, the test result is added to the condition record and marked as processed.

Conclusions

The Jennerfish system was able to process one month's worth of results from four of our five laboratories. The next step in assessment of the program is to begin parallel testing of matching each new case of a notifiable disease sent via existing notification pathways with the results from the Jennerfish system to determine whether it classifies results and cases as effectively as existing means. The list of diseases included in the Jennerfish database is broader than the list of notifiable diseases, so the epidemiological information generated is expected to be more extensive. The high number of new cases at the beginning will eventually decrease when time passes and more data is stored.